Draft genome sequences of obligate methylotrophs methylovorus sp. strain MM2 and Methylobacillus sp. strain MM3, isolated from grassland soil

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GENOME SEQUENCES

Draft Genome Sequences of Obligate Methylotrophs *Methylovorus* sp. Strain MM2 and *Methylobacillus* sp. Strain MM3, Isolated from Grassland Soil

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ABSTRACT Methylotrophs of the family *Methylophilaceae* were isolated from grassland soil. Here, we report the draft genome sequences of two obligate methylotrophs, *Methylovorus* sp. strain MM2 and *Methylobacillus* sp. strain MM3. These genome sequences provide further insights into the genetic and metabolic diversity of the *Methylophilaceae*.

The family *Methylophilaceae* is composed of four genera containing facultative and obligate methanol-utilizing methylotrophs (1–4). Members of the *Methylophilaceae* have been isolated from a range of locations, including terrestrial and marine environments (5–10). Here, we report the draft genome sequences of two obligate methylotrophs, *Methylovorus* sp. strain MM2 and *Methylobacillus* sp. strain MM3. The obligate nature of these methylotrophs was confirmed through growth experiments. The strains were isolated from soil collected at a 5-cm depth from grassland in Bawburgh, Norfolk, United Kingdom (52.6276 N, 1.1784 E).

Genome sequencing was performed by MicrobesNG using the Illumina MiSeq platform, producing 2 × 250-bp paired-end reads. Trimmed sequences were assembled using SPAdes version 3.7.1, and genome annotation was performed using the RAST annotation server (http://rast.nmpdr.org) (11, 12). Coverage of the genomes was calculated using BWA, SAMtools, and BEDTools genomecov (13–15). The *Methylovorus* sp. MM2 genome is composed of 27 contigs and includes 2,291 coding sequences (CDSs), 1 16S rRNA gene copy, and 46 tRNAs. The genome size is 2.42 Mb, with 46% G+C content. The genome of *Methylobacillus* sp. MM3, with 2.95 Mb and 57% G+C content, is composed of 64 contigs and includes 2,897 CDSs and 3 copies of 16S rRNA genes. Both genomes had 30-fold coverage.

Both genomes contain pyrroloquinoline quinone methanol dehydrogenases. *Methylobacillus* sp. MM3 possesses three separate gene clusters for the alternative methanol dehydrogenase XoxF (16, 17) and no copies of the canonical methanol dehydrogenase-encoding genes *mxaFI*. *Methylovorus* sp. MM2 possesses three copies of *xoxF* and one set of the genes *mxaFI*. All genes encoding the *N*-methylglutamate pathway for methylamine utilization (*mgdABC, gmaS*, and *mgsABC*) (18, 19) are present only in the genome of *Methylobacillus* sp. MM3, in addition to genes that encode dimethylamine dehydrogenase and trimethylamine dehydrogenase enzymes (*dmd* and *tmd*) (20, 21). The genes for an assimilatory nitrate reductase (*nasAB*) and the complete denitrification pathway (*narGHI, nirK, nirS, norB,* and *nosZ*) are present in the genome of *Methylobacillus* sp. MM3, while *Methylovorus* sp. MM2 possesses only an assimilatory nitrate reductase (*nasAB*) and a dissimilatory nitrite reductase (*nirBD*).

Data availability. These whole-genome shotgun projects have been deposited at DDBJ/ENA/GenBank under accession numbers LXTQ00000000 for *Methylobacillus* sp.

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MM3 and LXUF00000000 for *Methylovorus* sp. MM2. The versions described in this paper are the first versions. The strains are available from the authors upon request.

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